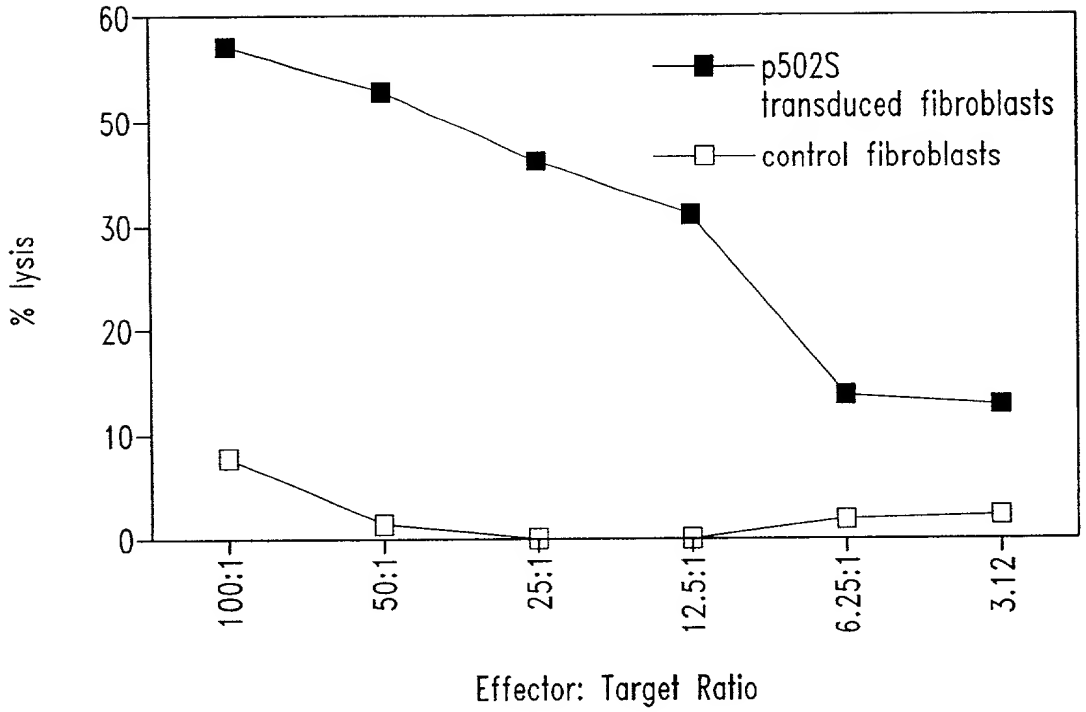

60
50
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

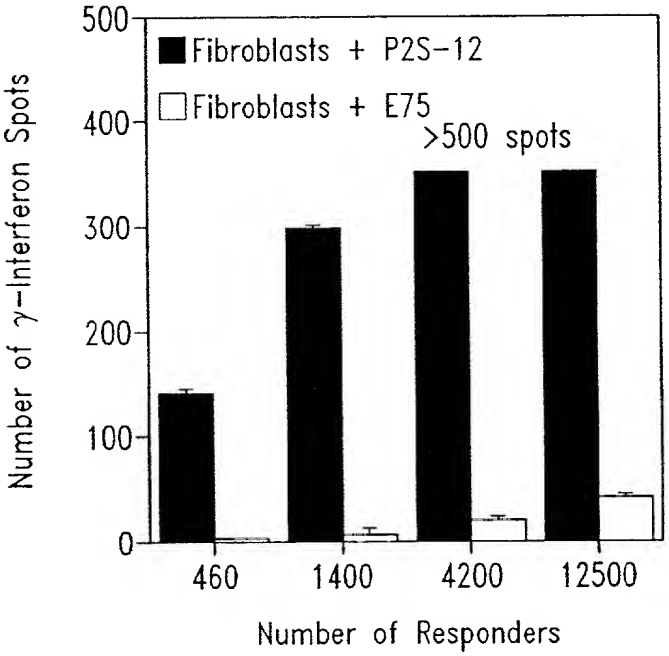

500
400
300
200
100
0
Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
460
1400
4200
12500
Number of Responders

Fig. 2A

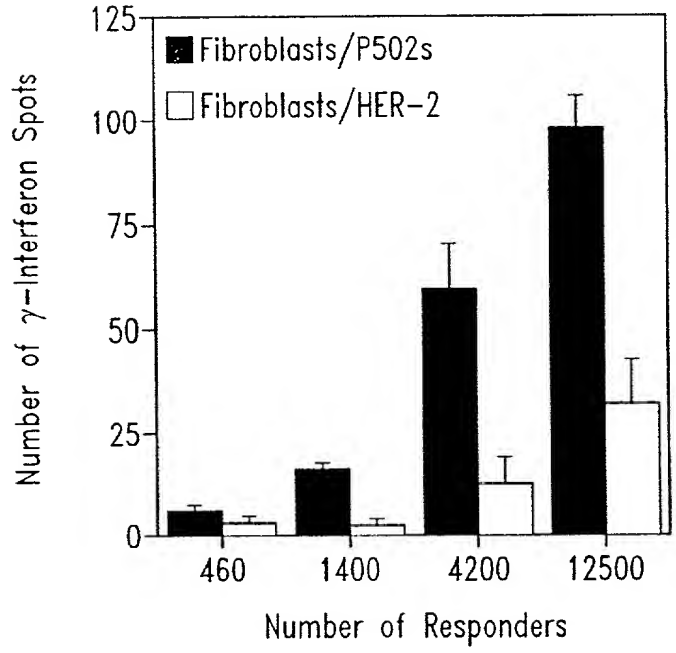

125
100
75
50
25
0
Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
460
1400
4200
12500
Number of Responders

Fig. 2B

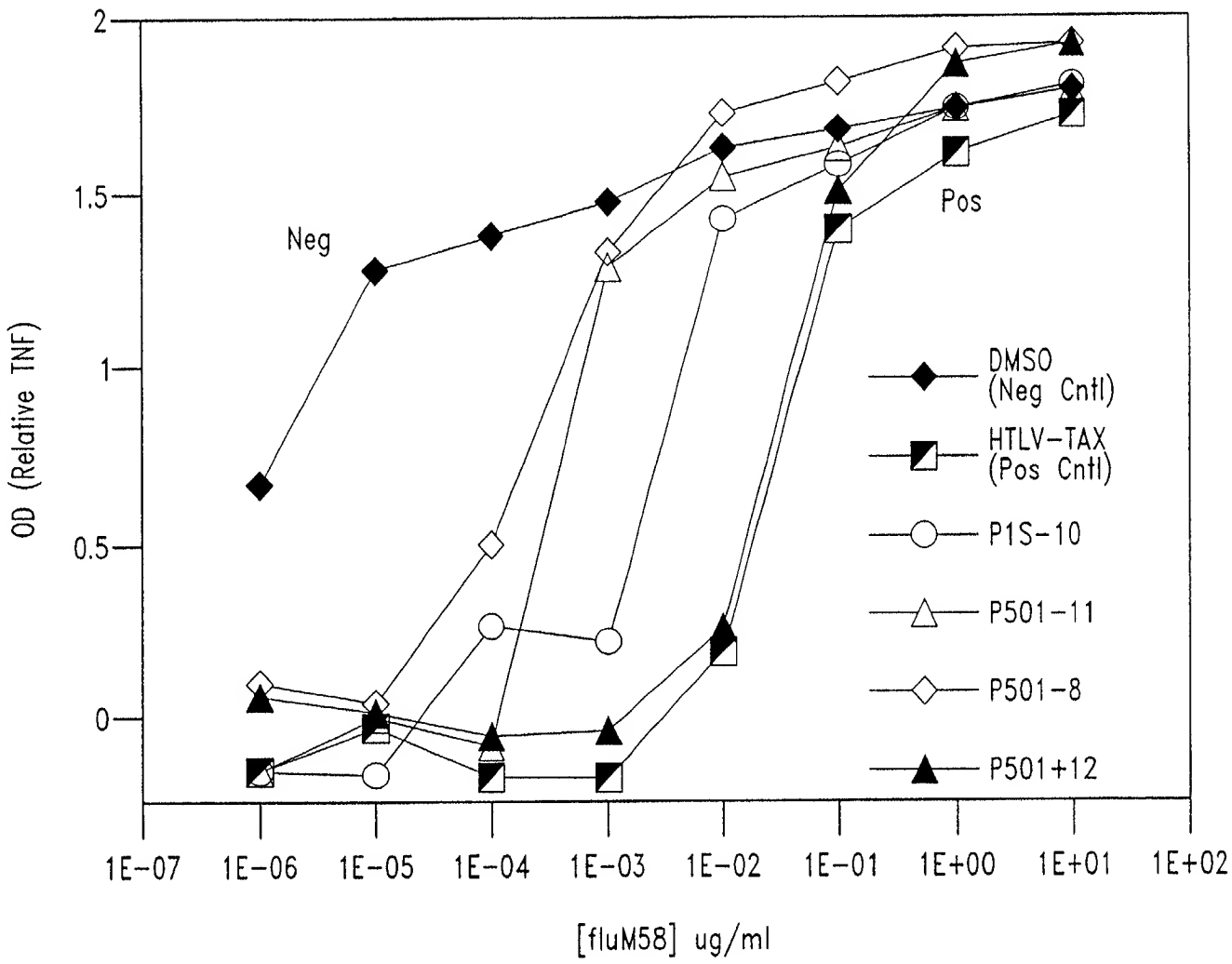


Fig. 3

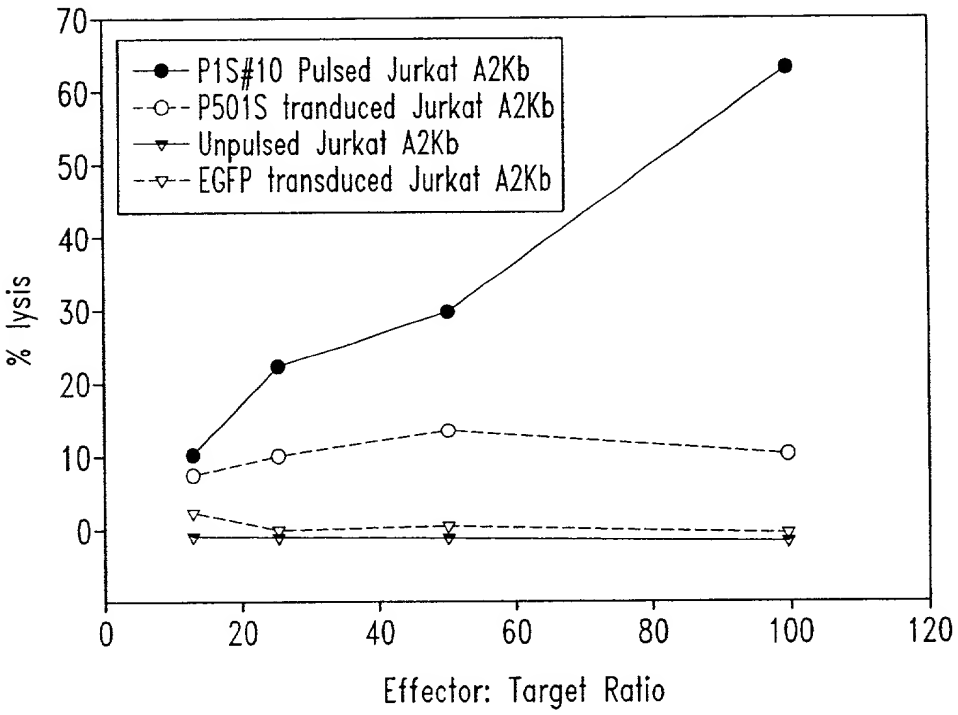

P1S#10 Pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Fig. 4

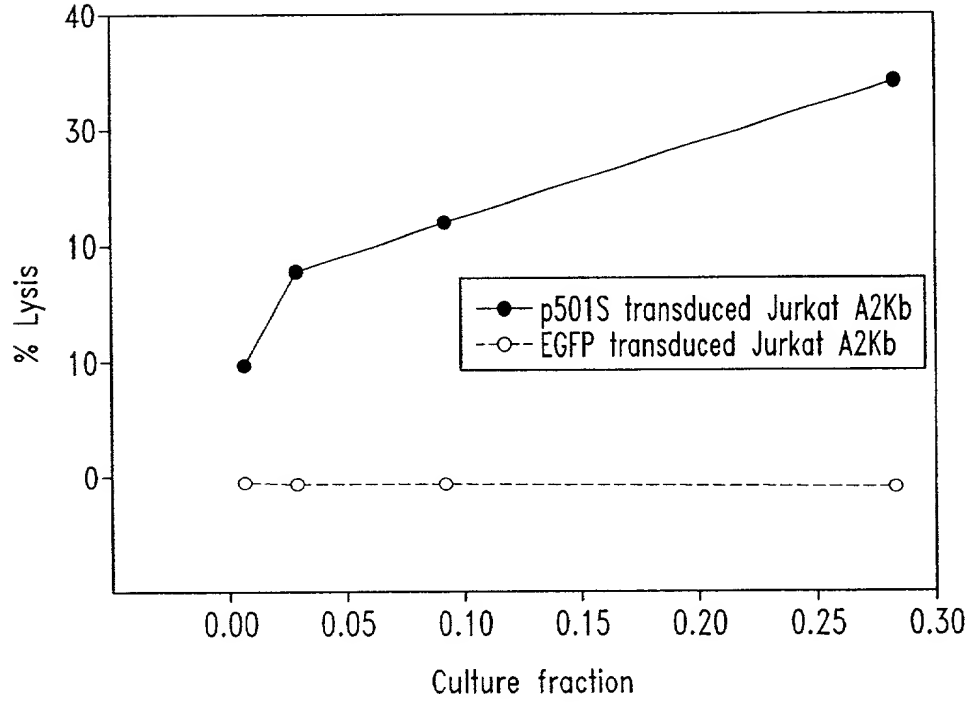

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
Culture fraction
0
10
10
30
40
0.00
0.05
0.10
0.15
0.20
0.25
0.30

Fig. 5

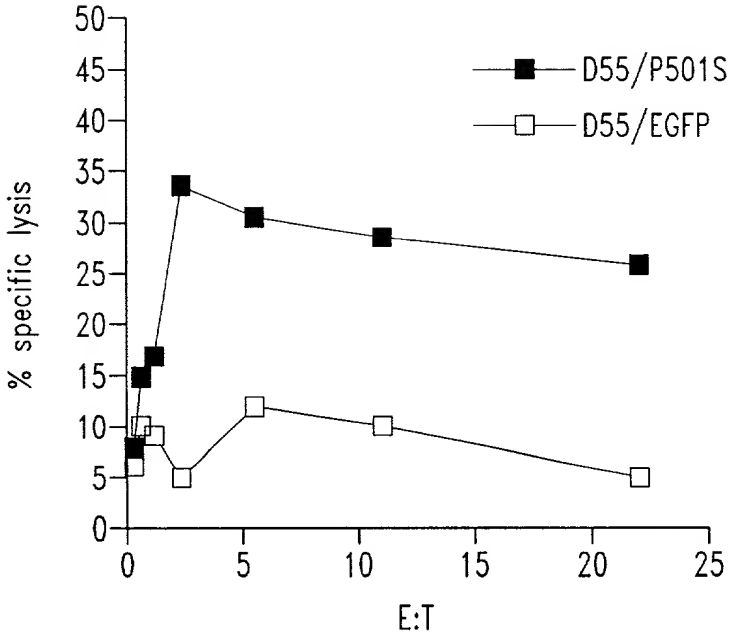

50
45
40
35
30
25
20
15
10
5
0
% specific lysis
0
5
10
15
20
25
E:T
D55/P501S
D55/EGFP

Fig. 6A

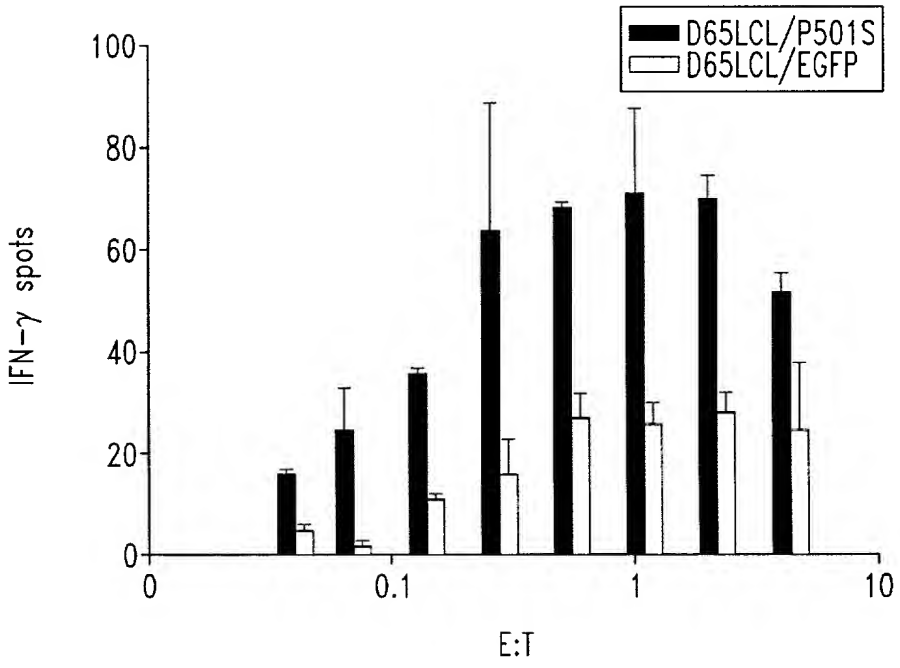
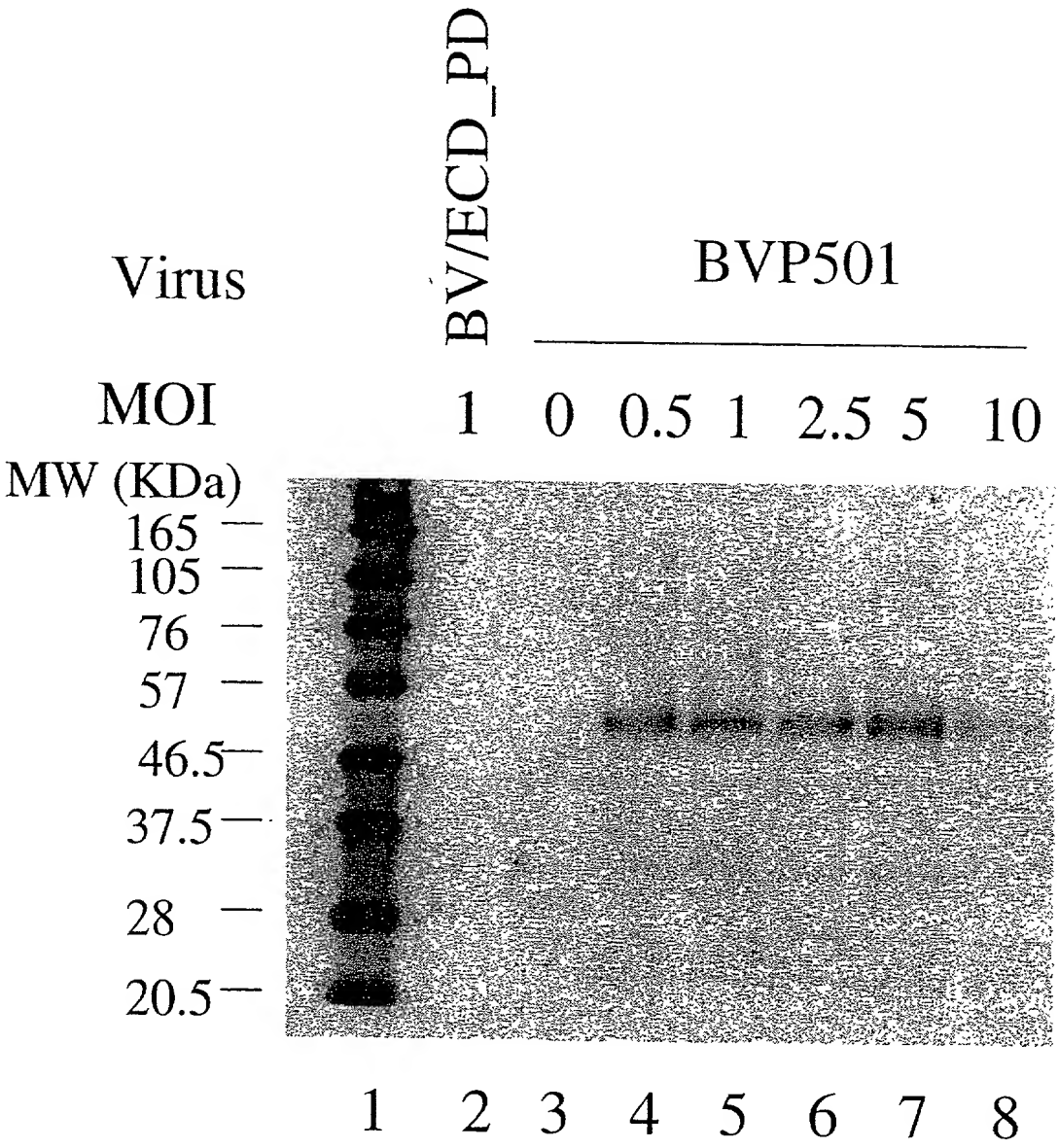

100
80
60
40
20
0
IFN-γ spots
0
0.1
1
10
E:T
D65LCL/P501S
D65LCL/EGFP

Fig. 6B

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 – 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

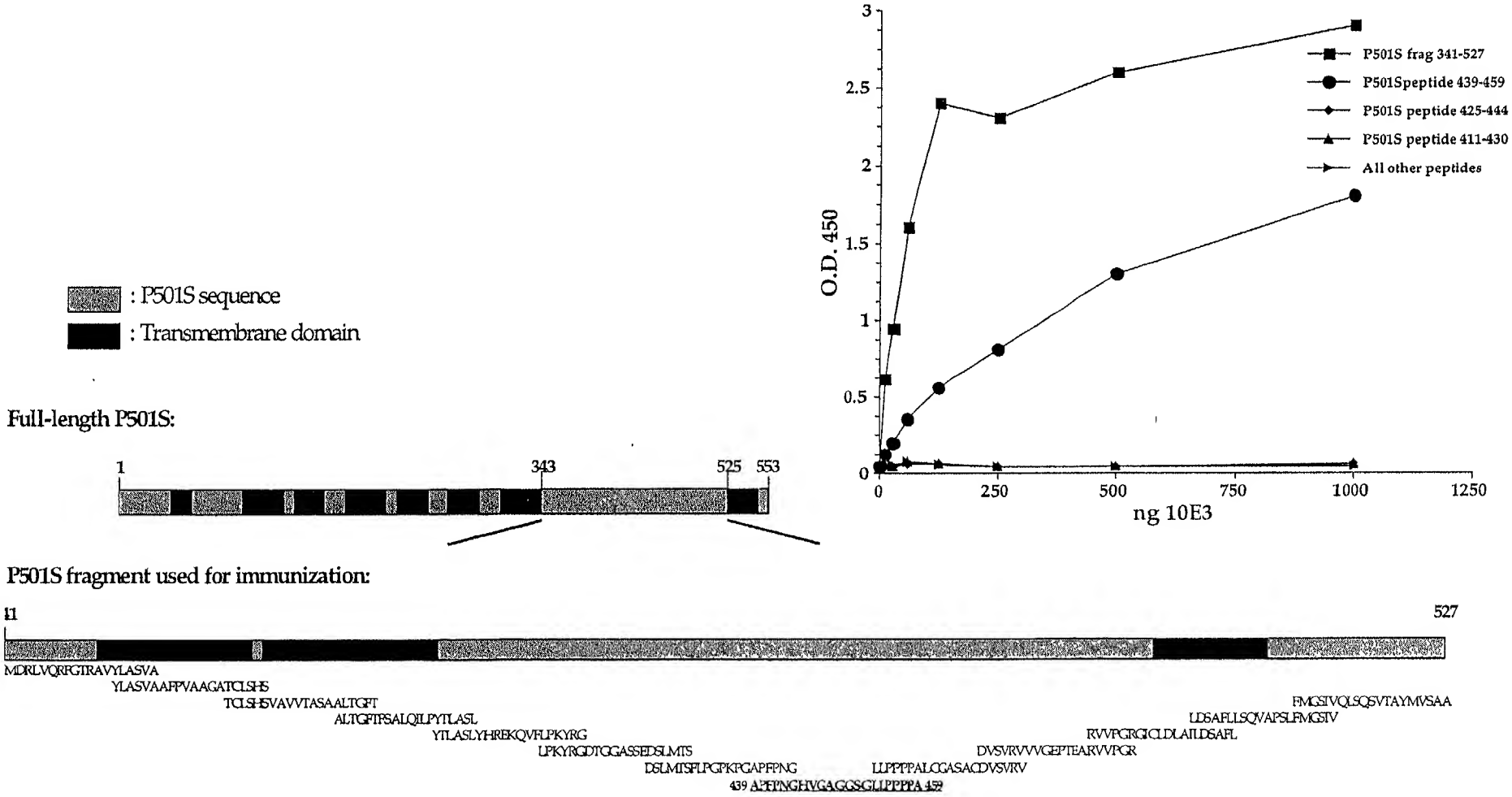


Fig. 8

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLAVVSRLLRHRK AQLLLYNLLTFGLEVCLAAGIT YVPPLLLEVGVEFKFM TMVLGIGPVLGLYCVPLLQSAS

DHWRGRVGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

FALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPYLGTQFE

CLPGLLTLIFLTCVAATLLY *AFFVATGPTFPVLGGSAPVLSPHCCPCRARIAFRNLGAILPRL*

HQLCCRMPRTLRR LPYAPLCSWMALMLFTLFYLDP VGEGLYQGVPLARPGTLARRHLYDRGVR

MGSLGLFLQCAISLVFSLVM *DRLVQREGTRAVYLAS* VAAFPYAAGATCLSHSVAVVTA SAA

LTGEFFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPKRG LCLDLAMLDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVALYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined, used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

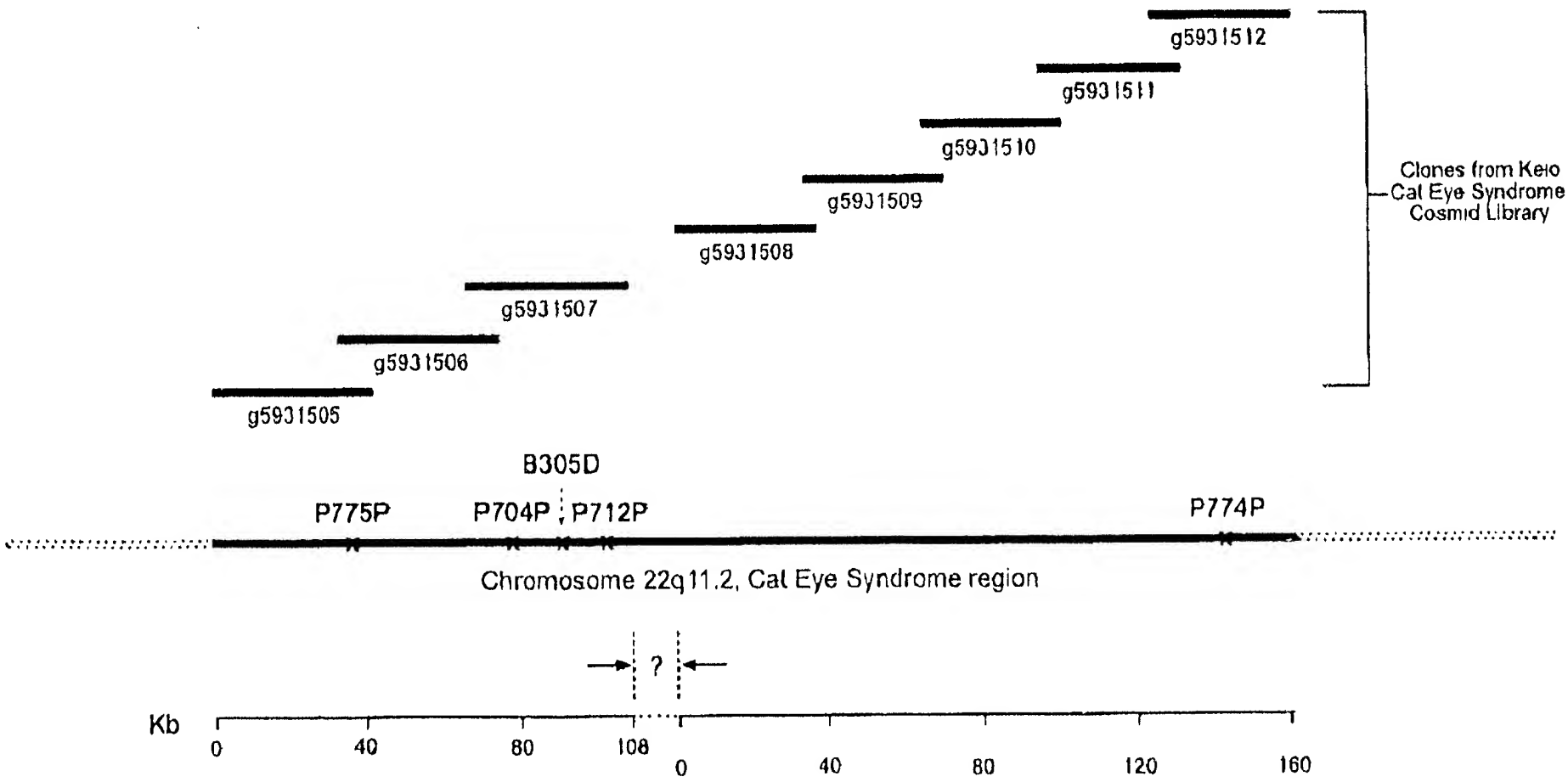


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

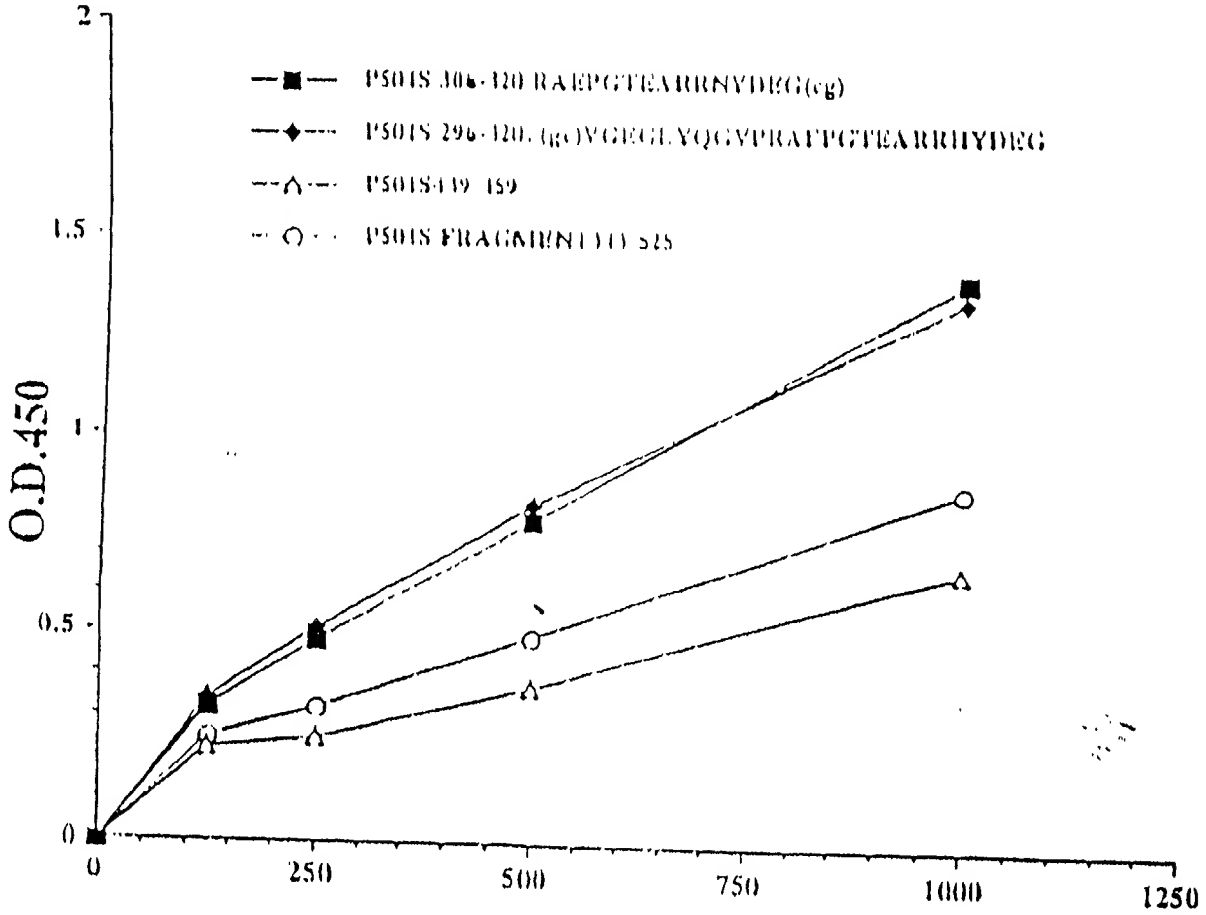


Fig. 11


10 20 30 40 50 60 70
GTCACTTAGGAAAAGGTGTCCTTTCGGGCAGCCGGGCTCAGCATGAGGAACAGAAGGAATGACACTCTGG 70
ACAGCACCCGGACCCTGTACTCCAGCGCGTCTCGGAGCACAGACTTGTCTTACACTGAAAGCGACTTGGT 140
GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
360 370 380 390 400 410 420
GAAGAAAGGGAAGTATATACGTCTGTCCTGCGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCACCTGAAAACA CCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAATATTGTGGCCATTGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATCAGGA 700
710 720 730 740 750 760 770
ATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACCACACACATTTGCTGCTGGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCA 840
AAGCTCCGGAATCAGCTAGAGGAAGCATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGA 910
TCCCCATTGTGTGTTTGCCCAAGGAGGTGGAAAAGAGACTTGAAGCCATCAATACCTCCATCAAAAA 980
TAAAATTCCTTGTGTGGTGGTGGAAGGCTCGGGCCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050
1060 1070 1080 1090 1100 1110 1120
GAGGATGCCCCGACATCTTCTGCCGTCAAGGAGAAGCTGGTGCGCTTTTTACCCGGCACGGTGTCCCGGC 1120
TGTCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTCTCGAATGTTCTCACCTATTAAC 1190
AGTTATTAAAATGGAAGAAGCTGGGGATGAAATTGTGAGCAATGCCATCTCCTACGCTCTATACAAAGCC 1260
TTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGCTGTTGAAGCTTCTGCTGGAGTGGAACCAGC 1330
TGGACTTAGCCAATGATGAGATTTCACCAATGACCGCCGATGGGAGTCTGCTGACCTTCAAGAAGTCAT 1400
1410 1420 1430 1440 1450 1460 1470
GTTTACGGCTCTCATAAAGGATAGACCCAAGTTTGTCGCCTCTTTCTGGAGAATGGCTTGAACCTACGG 1470
AAGTTTCTCACCCATGATGTCCTCACTGAACTCTTCTCCAAGCCACTTCAGCACGCTTGTGTACCGGAATC 1540
TGCAGATCGCCAAGAATTCCTATAATGATGCCCTCCTCACGTTTGTCTGGAAACTGGTTGCGAACTTCCG 1610
AAGAGGCTTCCGGAAGGAAGACAGAAATGGCGGGATGAGATGGACATAGAACTCCACGACGTGTCTCCT 1680
ATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAAG 1750
1760 1770 1780 1790 1800 1810 1820
TCATTTGGGAGCAGACCAGGGGCTGCACTCTGGCAGCCCTGCGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
CAAAGTGAAGAACGACATCAATGCTGCTGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCT 1890
GTTGAGCTGTTCACTGAGTGTTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTG 1960
AAGCTTGGGGTGGAAGCAACTGTCTGGAGCTGGCGGTGGAGGCCAGAGACCAGCATTTCACCGCCCAGCC 2030
TGGGGTCCAGAATTTCTTTCTAAGCAATGGTATGGAGATTTCCGAGACACCAAGAACTGGAAGATT 2100

Fig. 12A (1)


2110 2120 2130 2140 2150 2160 2170
TCCTGTGTCTGTTTATTATACCCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTCGACA 2170
AGCACAAGAAGCTGCTTTGGTACTATGTGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240
GGTCTTCTACATCGCCTTCCTCCTGCTGTTGCCTACGTGCTGCTCATGGATTTCCATTCGGTGCCACAC 2310
CCCCCCGAGCTGCTCCTGTACTCCCTGGTCTTTGTCCTCTTCTGTGATGAAGTCAGACAGTGGTACGTAA 2380
ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450
2460 2470 2480 2490 2500 2510 2520
AATTGTATTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTCTGGAC 2520
TACATTATTTTCACTCTAAGATTGATCCACATTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590
TGCTGCAGAGGATGCTGATCGATGTGTTCTTCTTCCTGTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660
CGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCCGTTCGGTCATCTAC 2730
GAGCCCTACCTGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGGTACCACGTATGACTTTGCCCACT 2800
2810 2820 2830 2840 2850 2860 2870
GCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCCGGTTCCC 2870
CGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940
GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGT 3010
ACTTCCTGGTGCAGGAGTACTGCAGCCGCCTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTA 3080
CATGGTGGTGAAGAAGTGCTTCAAGTGTTGCGCAGGAGAAAACATGGAGTCTTCTGTCTGCTGTTTC 3150
3160 3170 3180 3190 3200 3210 3220
AAAAATGAAGACAATGAGACTCTGGCATGGGAGGGTGTCATGAAGGAAAACTACCTTGTCAAGATCAACA 3220
CAAAAGCCAACGACACCTCAGAGGAAATGAGGCATCGATTTAGAGAACTGGATACAAAGCTTAATGATCT 3290
CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360
TAATTATAGCAAGATCATATTAAGGAATGCTGATGAACAATTTTGCTATCGACTACTAAATGAGAGATTT 3430
TCAGACCCCTGGGTACATGGTGGATGATTTAAATCACCCTAGTGTGCTGAGACCTTGAGAATAAAGTGT 3500
3510 3520 3530 3540 3550 3560 3570
GTGATTGGTTTCATACTTGAAGACGGATATAAAGGAAGAATATTTCCTTTATGTGTTTCTCCAGAATGGT 3570
GCCTGTTTGTCTCTGTGTCTCAATGCCTGGGACTGGAGGTTGATAGTTTAAGTGTGTTCTTACCGCCTCC 3640
TTTTTCCTTTAATCTTATTTTTGATGAACACA ATATAGGAGAACATCTATCCTATGAATAAGAACCTGG 3710
TCATGCTTTACTCCTGTATTGTATTTTGTTCATTCCAATTGATTCTCTACTTTTCCCTTTTTGTATT 3780
ATGTGACTAATTAGTTGGCATATTGTTAAAAGTCTCTCAAATTAGGCCAGATTCTAAAACATGCTGCAGC 3850
3860 3870 3880 3890 3900 3910 3920
AAGAGGACCCCGCTCTCTTCAGGAAAAGTGTTTTCATTCTCAGGATGCTTCTTACCTGTCAGAGGAGGT 3920
GACAAGGCAGTCTCTTGCTCTCTTGGACTCACCAGGCTCCTATTGAAGGAACCACCCCCATTCCTAAATA 3990
TGTGAAAAGTCGCCCAAAATGCAACCTTGAAAGGCACTACTGACTTTGTTCTTATTGGATACTCCTCTTA 4060
TTTATTATTTTTCCATTAAAAAAAATAGCTGGCTATTATAGAAAATTTAGACCATACAGAGATGTAGAAA 4130
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4210 4220 4230 4240 4250 4260 4270
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ATATCAATAATTGCATAATAGGCAACCTCTAGCGATTACCATAATTTGCTCATTGAAGGCTATCTCCAG 4410
TTGATCATTGGGATGAGCATCTTTGTGCATGAATCCTATTGCTGTATTTGGGAAAATTTTCCAAGGTTAG 4480
ATTCCAATAAATATCTATTTATTATTGAATATTAAAATATCGATTTATTATTAAAACCATTTATAAGGCT 4550

Fig. 12A(2)

4560 4570 4580 4590 4600 4610 4620

TTTTCATAAATGTATAGCAAATAGGAATTATTAACTTGAGCATAAGATATGAGATACATGAACCTGAACT 4620
ATTAAAATAAAATATTATATTTAACCCTAGTTTAAGAAGAAGTCAATATGCTTATTTAAATATTATGGAT 4690
GGTGGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACCACATCTCTACT 4760
AAAAATAAAAAAATTAGCTGGGTGTGGTGGTGCACTCCTGTAATCCCAGCTACTCAGAAGGCTGAGGTAC 4830
AAGAATTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCACTGCACTCCAGCCGGGG 4900

4910 4920 4930 4940 4950 4960 4970

TGACAGAGTGAGACTCCGACTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATATTATGG 4970
ATGGTGAAGGGAATGGTATAGAATTGGAGAGATTATCTTACTGAACACCTGTAGTCCCAGCTTTCTCTGG 5040
AAGTGGTGGTATTTGAGCAGGATGTGCACAAGGCAATTGAAATGCCCATAATTAGTTTCTCAGCTTTGAA 5110
TACACTATAAACTCAGTGGCTGAAGGAGGAAATTTTAGAAGGAAGCTACTAAAAGATCTAATTTGAAAAA 5180
CTACAAAAGCATTAACTAAAAAAGTTTATTTTCCTTTTGTCTGGGCAGTAGTGAAAATAACTACTCACAA 5250

5260 5270 5280 5290 5300 5310 5320

CATTCACTATGTTTGCAAGGAATTAACACAAATAAAAGATGCCTTTTTACTTAAACGCCAAGACAGAAAA 5320
CTTGCCCAATACTGAGAAGCAACTTGCATTAGAGAGGGAACTGTTAAATGTTTTCAACCCAGTTCATCTG 5390
GTGGATGTTTTTGCAGGTTACTCTGAGAATTTTGCTTATGAAAAATCATTATTTTTAGTGTAGTTCACAA 5460
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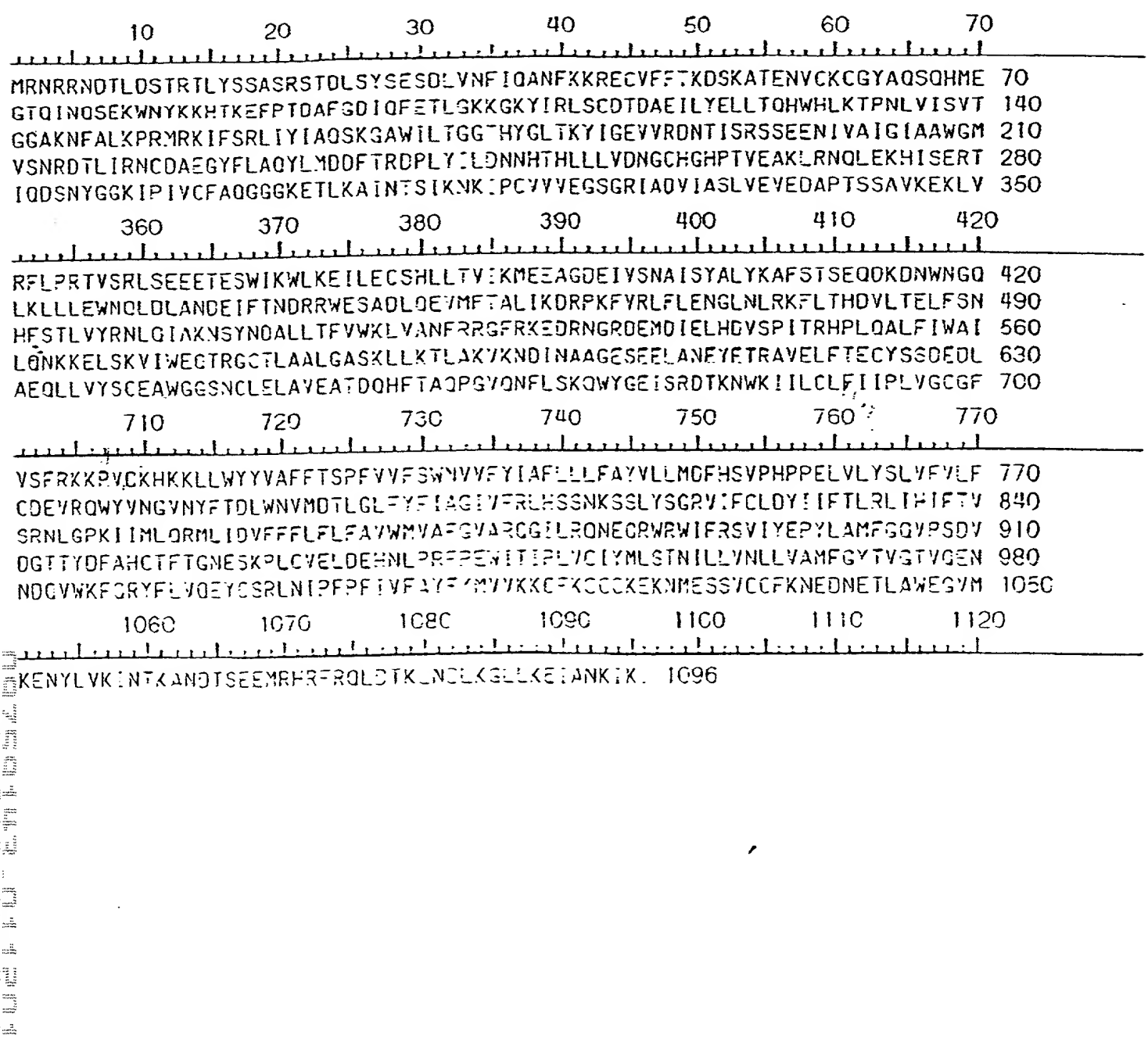
CTTTTGCACAACTGAGAATCCTGCGGCTTGGTTTAATGAGTGTGTTCATGAAATAAATAATGGAGGAATT 5600

5610 5620 5630 5640 5650 5660 5670

GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5668

Fig. 12A(3)


10 20 30 40 50 60 70
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GTQINQSEKWNYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT 140
GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM 210
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV 350
360 370 380 390 400 410 420
RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQQKDNWNGQ 420
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN 490
HFSTLVYRNLGIAKNSYNQALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI 560
LQNKKELSKVIWEGTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDL 630
AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPLVGCGF 700
710 720 730 740 750 760 770
VSFRKKPVCKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHPPELVLYSLVFVLF 770
CDEVRQWYVNGVNYFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTV 840
SRNLGPKIIMLQRMLIDVFFFLFLFAVWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDV 910
DGTTYDFAHCTFTGNESKPLCVELDEHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMFGYTVGTVQEN 980
NDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFAMVVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM 1050
1060 1070 1080 1090 1100 1110 1120
KENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKIK. 1096

Fig. 12B